<u>IN THE SPECIFICATION</u>:

Please amend the specification as follows:

At page 4, after "BRIEF DESCRIPTION OF THE DRAWINGS," please insert the following paragraph:

---The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.---

At pages 4 and 5, please substitute the description of Figures 1 to 4 with the following:

---- **Figure 1** shows the amino acid sequence of murine 1A6 antibody and human consensus sequence of heavy chain subgroup III (Humiii) and light chain kappa subgroup I. (SEQ ID NOS: 37 and 39, respectively). Asterisks denote amino acid differences between human and mouse sequence. CDR amino acids are in bold face.

Figure 2 shows a molecular model of humanized 1A6 (Hum B). **(A)** Side view of humB variable domains. Yellow: V_H; green: V_L; pale blue: CDRs; red: the six high risk "Vernier zone" residues and the V_H 60-64. **(B)** Top view of humB variable domains. Yellow: V_H; green: V_L; pale blue: CDRs; red: the six high risk "Vernier zone" residues and the V_H 60-64. **(C)** V_L49 and its surrounding residues. Magenta: ICAM-1; red: V_H and V_L residues; blue: residues at V_H-V_L interphase; purple: W102 in V_H.

Figure 3 shows the amino acid sequence of murine 1A6 antibody, humanized 1A6 (HumB) and human consensus sequences of heavy chain subgroup III (Humiii) (SEQ ID NOS: 37 and 39, respectively) and light chain kappa subgroup I (SEQ ID NOS: 38 and 40, respectively). Asterisks and bold face amino acids are as previously indicated.

Figure 4 shows the cDNA sequence of humanized scFV3 (HumA) antibody (SEQ ID NO: 47). Restriction sites are indicated by underlining.---

At pages 36 to 46, please substitute the detailed description with the following description sections:

---Finally, molecular model building indicates that a portion of the CDR2 in the VH domain, VH60-64, does not have direct contact with the antigen. Therefore mouse residues at these positions (DPKVQ) (piece of SEQ ID NO: 17) can be replaced by human residues ADSVK (piece of SEQ ID NO: 1).

<u>Example 2</u>

This example describes the preparation of several humanized scFv expression constructs.

The humanized scFv A (HumA) cDNA (FIG. 4)(SEQ ID NO: 47) containing 750 bb was synthesized using a series of overlapping oligonucleotides. These overlapping oligonucleotides (Table 1) were designed to encode the amino acids of the variable region of the heavy (V_H) and light (V_L) chains linked by a linker((G_4S)$_4$)(SEQ ID NO: 96) with a Bam H1 site. The heavy chain and light chain were cloned separately in TOPO 2.1 vector. After DNA sequencing conformation, the heavy and light chain were subcloned into expression vector (pBAD/pIII A) to form full length DNA.

The oligonucleotides were first annealed in six groups consisting of oligo AVH1/AVH2, oligo AVH3/AVH4, oligo AVH5/AVH6 for heavy chain, and oligo AVL1/AVL2, oligo AVL3/AVL4, oligo AVL5/AVL6 for the light chain. Each annealed group was extended with the Klenow fragment of DNA polymerase. The annealed and extended products of group 1-3 were pooled with oligo AVH7 as overlapping templates that were amplified via polymerase chain reaction (PCR) using the high-fidelity thermostable DNA polymerase (Roche) with oligo AVH8 and AVH9 as primers. The annealed and extended products of group 4-6 were pooled with oligo AVL7 as overlapping templates that were also amplified via polymerase chain reaction (PCR) using oligo AVL8 and AVL9 as primers. The PCR products were directly inserted into the TA cloning vector pCR2.1-TOPO (Invitrogen) and transferred into TOP10 competent cells. The plasmids with inserts were isolated and sequenced.

The light chain and the heavy chain DNA fragments were isolated from their cloning vector by digestion with Nco I/Bam H I and Bam H I/Hpa I respectively, and cloned into expression vector pBAD/pIII A cutting with Nco I / Sal I (blunted) to be in frame with the

carboxy-terminal His tag. Both strands of the expression construct pBAD-HumA was sequenced (MWG Biotech, Inc.).

All other human scFv expression constructs (HumB to H) were made with the same procedure as HumA described above except using different oligonucleotides (Table 1).

For HumB, using BVH6 and BVH7 to replace AVH6 and AVH7; for HumC, using CVH5, CVH6 and CVH7 to replace AVH5, AVH6 and AVH7; for HumD, using DVH6 and DVH7 to replace AVH6 and AVH7; for HumE, using EVH4, EVH5, EVH6 and EVH7 to replace AVH4, AVH5, AVH6 and AVH7; for HumF, using FVH6 and FVH7 to replace AVH6 and AVH7; for HumG, using GVL3, GVL4, GVH5, GVH6 and GVH7 to replace AVL3, AVL4, AVH5, AVH6 and AVH7; for HumH, using HVL3, HVL4, HVH4, HVH5, HVH6 and HVH7 to replace AVL3, AVL4, AVH4, AVH5, AVH6 and AVH7; for HumI, using IVL3, IVL4, IVH4, IVH5, IVH6 and IVH7 to replace AVL3, AVL4, AVH4, AVH5, AVH6 and AVH7.

Table 1. Oligonucleotides for humanized scFvs

Oligonucleotides for the light (V_H) chain of HumA:

AVL-1:(SEQ ID NO: 48)
CGAACCATGGGCGATATCCAGATGACCCAATCTCCGTCTAGCCTGAGCGCCAGTGTTGGTG
AVL-2: (SEQ ID NO: 49)
GTGAAGATTATTACTGATAGATTGGCTGGCGCGGCAAGTAATGGTAACTCGATCACCAACACTGGCGCTCAG
AVL-3: (SEQ ID NO: 50)
CTATCAGTAATAATCTTCACTGGTATCAACAAAAACCGGGTAAAGCTCCGAAACTTCTTATCTATCACGCC
AVL-4: (SEQ ID NO: 51)
CCCGAGCCAGAGCCAGAGAAGCGGCTCGGAACGCCGCTAATGCTCTGAGAGGCGTGATAGATAAGAAG
AVL-5: (SEQ ID NO: 52)
CTCTGGCTCTGGCTCGGGCACGGACTTTACCCTTACCATCAGCTCTCTTCAGCCGGAAGACTTTGCCACC
AVL-6: (SEQ ID NO: 53)
CCTTGACCGAAGGTATACGGCCAGCTATTAGACTGCTGACAATAATAGGTGGCAAAGTCTTCCGGC
AVL-7: (SEQ ID NO: 54)
GTATACCTTCGGTCAAGGTACCAAGGTCGAGATTAAGCGCGGCGGTGGCGGTTCTGGTGGCGGTGGTAGCG
AVL-8: (SEQ ID NO: 55)
CGAACCATGGGCGATATCCAGATGACCCAATC

AVL-9: (SEQ ID NO: 56)
CGGATCCACCGCCACCGCTACCACCGCCACCAG

Oligonucleotides for the heavy (V_H) chain of HumA:

AVH-1: (SEQ ID NO: 57)
GGTGGCGGTGGATCCGGTGGCGGTGGCAGCGAAGTTCAACTTGTTGAGTCTGGTGGCGGTCTGGT
TCAGCCGG
AVH-2: (SEQ ID NO: 58)
GTCCTTAATGTTGAAACCGCTTGCTGCGCAAGACAGGCGCAGAGAGCCACCCGGCTGAACCAGACC
GCCAC
AVH-3: (SEQ ID NO: 59)
GGTTTCAACATTAAGGACACCTACATCCATTGGGTGAGGCAAGCTCCGGGTAAGGGTCTGGAGTGG
G
AVH-4: (SEQ ID NO: 60)
GGCCCTTCACGCTGTCAGCGTAAATGGTGTTGTCGTTTGCCGGGTCGATACGTGCCACCCACTCCA
GACCCTTACC
AVH-5: (SEQ ID NO: 61)
CGCTGACAGCGTGAAGGGCCGTTTTACTATTTCTAGCGACGACTCTAAGAACACCGCGTACCTTCAG
ATGAACTCTCTGCG
AVH-6(SEQ ID NO: 62)
CCAGTAGCCAGAGTCCGTGCAGTAGTAGACGGCGGTGTCCTCGGCACGCAGAGAGTTCATCTGAAG
G
AVH-7: (SEQ ID NO: 63)
GGACTCTGGCTACTGGTTTGCCTACTGGGGCCAGGGCACGCTTGTCACCGTCTCTTCTGGTTAAC
AVH-8: (SEQ ID NO: 64)
GGTGGCGGTGGATCCGGT
AVH-9: (SEQ ID NO: 65)
GGGTTAACCAGAAGAGACGG

Oligonucleotides for making other human scFv (Hum B-I):
BVH-6: (SEQ ID NO: 66)
CCAGTAGCCAGAGGCCGTGCAGTAGTAGACGGCGGTGTCCTCGGCACGCAGAGAGTTCATCTGAA
GG
BVH-7: (SEQ ID NO: 67)
GGCCTCTGGCTACTGGTTTGCCTACTGGGGCCAGGGCACGCTTGTCACCGTCTCTTCTGGTTAAC
CVH-5: (SEQ ID NO: 68)
CGCTGACAGCGTGAAGGGCCGTTTTACTATTTCTGGCGACGACTCTAAGAACACCGCGTACCTTCAG
ATGAACTCTCTGCG
CVH-6: (SEQ ID NO: 69)
CCAGTAGCCAGAGGTCGTGCAGTAGTAGACGGCGGTGTCCTCGGCACGCAGAGAGTTCATCTGAAG
G
CVH-7: (SEQ ID NO: 70)
GACCTCTGGCTACTGGTTTGCCTACTGGGGCCAGGGCACGCTTGTCACCGTCTCTTCTGGTTAAC
DVH-6: (SEQ ID NO: 71)
CCAGTAGCCAGAGGTCGTGCAGTAGTAGACGGCGGTGTCCTCGGCACGCAGAGAGTTCATCTGAAG
G
DVH-7: (SEQ ID NO: 72)
GACCTCTGGCTACTGGTTTGCCTACTGGGGCCAGGGCACGCTTGTCACCGTCTCTTCTGGTTAAC
EVH-4: (SEQ ID NO: 73)
GGCCCTGCACCTTCGGATCGTAAATGGTGTTGTCGTTTGCCGGGTCGATACGTGCCACCCACTCCA
GACCCTTACC
EVH-5: (SEQ ID NO: 74)
CGATCCGAAGGTGCAGGGCCGTTTTACTATTTCTGCGGACGACTCTAAGAACACCGCGTACCTTCAG
ATGAACTCTCTGCG
EVH-6: (SEQ ID NO: 75)
CCAGTAGCCAGAGGTCGTGCAGTAGTAGACGGCGGTGTCCTCGGCACGCAGAGAGTTCATCTGAAG
G

5

EVH-7: (SEQ ID NO: 76)
GACCTCTGGCTACTGGTTTGCCTACTGGGGCCAGGGCACGCTTGTCACCGTCTCTTCTGGTTAAC
FVH-6: (SEQ ID NO: 77)
CCAGTAGCCAGAGGTCGTGCAGTAGTAGACGGCGGTGTCCTCGGCACGCAGAGAGTTCATCTGAAG
G
FVH-7: (SEQ ID NO: 78)
GACCTCTGGCTACTGGTTTGCCTACTGGGGCCAGGGCACGCTTGTCACCGTCTCTTCTGGTTAAC
GVL-3: (SEQ ID NO: 79)
CTATCAGTAATAATCTTCACTGGTATCAACAAAAACCGGGTAAAGCTCCGAAACTTCTTATCAAACAC
GCC
GVL-4: (SEQ ID NO: 80)
CCCGAGCCAGAGCCAGAGAAGCGGCTCGGAACGCCGCTAATGCTCTGAGAGGCGTGAAAGATAAG
AAG
GVH-5: (SEQ ID NO: 81)
CGCTGACAGCGTGAAGGGCCGTTTTACTATTTCTGCGGACGACTCTAAGAACACCGCGTACCTTCAG
ATGAACTCTCTGCG
GVH-6: (SEQ ID NO: 82)
CCAGTAGCCAGAGGTCGTGCAGTAGTAGACGGCGGTGTCCTCGGCACGCAGAGAGTTCATCTGAAG
G
GVH-7: (SEQ ID NO: 83)
GACCTCTGGCTACTGGTTTGCCTACTGGGGCCAGGGCACGCTTGTCACCGTCTCTTCTGGTTAAC
HVL-3: (SEQ ID NO: 84)
CTATCAGTAATAATCTTCACTGGTATCAACAAAAACCGGGTAAAGCTCCGAAACTTCTTATCAAACAC
GCC
HVL-4: (SEQ ID NO: 85)
CCCGAGCCAGAGCCAGAGAAGCGGCTCGGAACGCCGCTAATGCTCTGAGAGGCGTGAAAGATAAG
AAG
HVH-4: (SEQ ID NO: 86)
GGCCCTGCACCTTCGGATCGTAAATGGTGTTGTCGTTTGCCGGGTCGATACGTGCCACCCACTCCA
GACCCTTACC
HVH-5: (SEQ ID NO: 87)
CGATCCGAAGGTGCAGGGCCGTTTTACTATTTCTGCGGACGACTCTAAGAACACCGCGTACCTTCAG
ATGAACTCTCTGCG
HVH-6: (SEQ ID NO: 88)
CCAGTAGCCAGAGGTCGTGCAGTAGTAGACGGCGGTGTCCTCGGCACGCAGAGAGTTCATCTGAAG
G
HVH-7: (SEQ ID NO: 89)
GACCTCTGGCTACTGGTTTGCCTACTGGGGCCAGGGCACGCTTGTCACCGTCTCTTCTGGTTAAC
IVL-3: (SEQ ID NO: 90)
CTATCAGTAATAATCTTCACTGGTATCAACAAAAACCGGGTAAAGCTCCGAAACTTCTTATCAAACAC
GCC
IVL-4: (SEQ ID NO: 91)
CCCGAGCCAGAGCCAGAGAAGCGGCTCGGAACGCCGCTAATGCTCTGAGAGGCGTGAAAGATAAG
AAG
IVH-4: (SEQ ID NO: 92)
GGCCCTGCACCTTCGGATCGTAAATGGTGTTGTCGTTTGCCGGGTCGATACGTGCCACCCACTCCA
GACCCTTACC
IVH-5: (SEQ ID NO: 93)
CGATCCGAAGGTGCAGGGCCGTTTTACTATGTCTGCGGACACCTCTAAGAACACCGCGTACCTTCA
GATGAACTCTCTGCG
IVH-6: (SEQ ID NO: 94)
CCAGTAGCCAGAGGTCGTGCAGTAGTAGACGGCGGTGTCCTCGGCACGCAGAGAGTTCATCTGAAG
G
IVH-7: (SEQ ID NO: 95)
GACCTCTGGCTACTGGTTTGCCTACTGGGGCCAGGGCACGCTTGTCACCGTCTCTTCTGGTTAAC

Molecular model building enabled synthesis of 9 versions of humanized antibodies in the form of scFv (HumA-HumI, summarized in Tables 2 and 3). Four of the humanized antibodies, HumA-HumD, do not have parental mouse framework residues, and five of them, HumE-HumI, contain various number of parental mouse residues in the framework. The sequence of HumB is compared against parental mouse 1A6 and human consensus framework in FIG. 3.

Table 2. Humanization Constructs

Position	L49	H37	H60-64	H69	H71	H73	H94
Human / Mouse	Y/K	V/M	ADSVK/DPKVQ	I/M	R/A	D/T	R/T
HumA	Y	V	ADSVK	I	S	D	D
HumB	Y	V	ADSVK	I	S	D	A
HumC	Y	V	ADSVK	I	G	D	T
HumD	Y	V	ADSVK	I	S	D	T
HumE	Y	V	DPKVQ	I	A	D	T
HumF	Y	V	ADSVK	I	A	D	T
HumG	K	V	ADSVK	I	A	D	T
HumH	K	V	DPKVQ	I	A	D	T
HumI	K	M	DPKVQ	M	A	T	T

(ADSVK is piece of SEQ ID NO 1; DPKVQ is a piece of SEQ ID NO: 17.)

Table 3. Amino Acid Sequences of Humanized Antibody

Hum A:

VH Domain (SEQ ID NO: 1)

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
Ala Ala Ser (Gly Phe Asn Ile Lys Asp Thr Tyr Ile His) Trp Val Arg Gln Ala Pro Gly Lys Gly
Leu Glu Trp Val Ala (Arg Ile Asp Pro Ala Asn Asp Asn Thr Ile Tyr Ala Asp Ser Val Lys Gly)
Arg Phe Thr Ile Ser Ser Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala

Glu Asp Thr Ala Val Tyr Tyr Cys Thr Asp (Ser Gly Tyr Trp Phe Ala Tyr) Trp Gly Gln Gly Thr

Leu Val Thr Val Ser Ser

VL Domain (SEQ ID NO: 3)

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys

(Arg Ala Ser Gln Ser Ile Ser Asn Asn Leu His) Trp Tyr Gln Gln Lys Pro

Gly Lys Ala Pro Lys Leu Leu Ile Tyr (His Ala Ser Gln Ser Ile Ser) Gly Val Pro Ser

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

Glu Asp Phe Ala Thr Tyr Tyr Cys (Gln Gln Ser Asn Ser Trp Pro Tyr Thr) Phe Gly Gln

Gly Thr Lys Val Glu Ile Lys Arg

Hum B:

VH Domain (SEQ ID NO: 5)
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu

Ser Cys Ala Ala Ser (Gly Phe Asn Ile Lys Asp Thr Tyr Ile His) Trp Val Arg Gln Ala

Pro Gly Lys Gly Leu Glu Trp Val Ala (Arg Ile Asp Pro Ala Asn Asp Asn Thr Ile Tyr Ala

Asp Ser Val Lys Gly) Arg Phe Thr Ile Ser Ser Asp Asp Ser Lys Asn Thr Ala Tyr Leu

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ala (Ser Gly Tyr Trp Phe

Ala Tyr) Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

VL Domain (SEQ ID NO: 7)
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr

Ile Thr Cys (Arg Ala Ser Gln Ser Ile Ser Asn Asn Leu His) Trp Tyr Gln Gln Lys Pro

Gly Lys Ala Pro Lys Leu Leu Ile Tyr (His Ala Ser Gln Ser Ile Ser) Gly Val Pro Ser

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

Glu Asp Phe Ala Thr Tyr Tyr Cys (Gln Gln Ser Asn Ser Trp Pro Tyr Thr) Phe Gly Gln

Gly Thr Lys Val Glu Ile Lys Arg

Hum C:
VH Domain (SEQ ID NO: 9)
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu

Ser Cys Ala Ala Ser (Gly Phe Asn Ile Lys Asp Thr Tyr Ile His) Trp Val Arg Gln Ala

Pro Gly Lys Gly Leu Glu Trp Val Ala (Arg Ile Asp Pro Ala Asn Asp Asn Thr Ile Tyr Ala

Asp Ser Val Lys Gly) Arg Phe Thr Ile Ser Gly Asp Asp Ser Lys Asn Thr Ala Tyr Leu

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Thr (Ser Gly Tyr Trp Phe
Ala Tyr) Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

VL Domain (SEQ ID NO: 11)
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr

Ile Thr Cys (Arg Ala Ser Gln Ser Ile Ser Asn Asn Leu His) Trp Tyr Gln Gln Lys Pro

Gly Lys Ala Pro Lys Leu Leu Ile Tyr (His Ala Ser Gln Ser Ile Ser) Gly Val Pro Ser

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

Glu Asp Phe Ala Thr Tyr Tyr Cys (Gln Gln Ser Asn Ser Trp Pro Tyr Thr) Phe Gly Gln

Gly Thr Lys Val Glu Ile Lys Arg

Hum D:
VH Domain (SEQ ID NO: 13)
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu

Ser Cys Ala Ala Ser (Gly Phe Asn Ile Lys Asp Thr Tyr Ile His) Trp Val Arg Gln Ala
Pro Gly Lys Gly Leu Glu Trp Val Ala (Arg Ile Asp Pro Ala Asn Asp Asn Thr Ile Tyr Ala

Asp Ser Val Lys Gly) Arg Phe Thr Ile Ser Ser Asp Asp Ser Lys Asn Thr Ala Tyr Leu

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Thr (Ser Gly Tyr Trp Phe
Ala Tyr) Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

VL Domain (SEQ ID NO: 15)
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr

Ile Thr Cys (Arg Ala Ser Gln Ser Ile Ser Asn Asn Leu His) Trp Tyr Gln Gln Lys Pro

Gly Lys Ala Pro Lys Leu Leu Ile Tyr (His Ala Ser Gln Ser Ile Ser) Gly Val Pro Ser

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

Glu Asp Phe Ala Thr Tyr Tyr Cys (Gln Gln Ser Asn Ser Trp Pro Tyr Thr) Phe Gly Gln

Gly Thr Lys Val Glu Ile Lys Arg

9

Hum E:
VH Domain (SEQ ID NO: 17)
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu

Ser Cys Ala Ala Ser (Gly Phe Asn Ile Lys Asp Thr Tyr Ile His) Trp Val Arg Gln Ala

Pro Gly Lys Gly Leu Glu Trp Val Ala (Arg Ile Asp Pro Ala Asn Asp Asn Thr Ile Tyr Asp Pro

Lys Val Gln Gly) Arg Phe Thr Ile Ser Ala Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn

Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Thr (Ser Gly Tyr Trp Phe Ala Tyr) Trp

Gly Gln Gly Thr Leu Val Thr Val Ser Ser

VL Domain (SEQ ID NO: 19)
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr

Ile Thr Cys (Arg Ala Ser Gln Ser Ile Ser Asn Asn Leu His) Trp Tyr Gln Gln Lys Pro

Gly Lys Ala Pro Lys Leu Leu Ile Tyr (His Ala Ser Gln Ser Ile Ser) Gly Val Pro Ser

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

Glu Asp Phe Ala Thr Tyr Tyr Cys (Gln Gln Ser Asn Ser Trp Pro Tyr Thr) Phe Gly Gln

Gly Thr Lys Val Glu Ile Lys Arg

Hum F:
VH Domain (SEQ ID NO: 21)
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu

Ser Cys Ala Ala Ser (Gly Phe Asn Ile Lys Asp Thr Tyr Ile His) Trp Val Arg Gln Ala

Pro Gly Lys Gly Leu Glu Trp Val Ala (Arg Ile Asp Pro Ala Asn Asp Asn Thr Ile Tyr Ala

Asp Ser Val Lys Gly) Arg Phe Thr Ile Ser Ala Asp Asp Ser Lys Asn Thr Ala Tyr Leu

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Thr (Ser Gly Tyr Trp Phe

Ala Tyr) Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

VL Domain (SEQ ID NO: 23)
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr

Ile Thr Cys (Arg Ala Ser Gln Ser Ile Ser Asn Asn Leu His) Trp Tyr Gln Gln Lys Pro

Gly Lys Ala Pro Lys Leu Leu Ile Tyr (His Ala Ser Gln Ser Ile Ser) Gly Val Pro Ser

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

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Glu Asp Phe Ala Thr Tyr Tyr Cys (Gln Gln Ser Asn Ser Trp Pro Tyr Thr) Phe Gly Gln

Gly Thr Lys Val Glu Ile Lys Arg

Hum G:
VH Domain (SEQ ID NO: 25)
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu

Ser Cys Ala Ala Ser (Gly Phe Asn Ile Lys Asp Thr Tyr Ile His) Trp Val Arg Gln Ala

Pro Gly Lys Gly Leu Glu Trp Val Ala (Arg Ile Asp Pro Ala Asn Asp Asn Thr Ile Tyr Ala

Asp Ser Val Lys Gly) Arg Phe Thr Ile Ser Ala Asp Asp Ser Lys Asn Thr Ala Tyr Leu

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Thr (Ser Gly Tyr Trp Phe
Ala Tyr) Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

VL Domain (SEQ ID NO: 27)
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
Ile Thr Cys (Arg Ala Ser Gln Ser Ile Ser Asn Asn Leu His) Trp Tyr Gln Gln Lys Pro

Gly Lys Ala Pro Lys Leu Leu Ile Lys (His Ala Ser Gln Ser Ile Ser) Gly Val Pro Ser

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

Glu Asp Phe Ala Thr Tyr Tyr Cys (Gln Gln Ser Asn Ser Trp Pro Tyr Thr) Phe Gly Gln

Gly Thr Lys Val Glu Ile Lys Arg

Hum H:
VH Domain (SEQ ID NO: 29)
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu

Ser Cys Ala Ala Ser (Gly Phe Asn Ile Lys Asp Thr Tyr Ile His) Trp Val Arg Gln Ala

Pro Gly Lys Gly Leu Glu Trp Val Ala (Arg Ile Asp Pro Ala Asn Asp Asn Thr Ile Tyr Asp Pro
Lys Val Gln Gly) Arg Phe Thr Ile Ser Ala Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn
Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Thr (Ser Gly Tyr Trp Phe Ala Tyr) Trp
Gly Gln Gly Thr Leu Val Thr Val Ser Ser

VL Domain (SEQ ID NO: 31)
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr

Ile Thr Cys (Arg Ala Ser Gln Ser Ile Ser Asn Asn Leu His) Trp Tyr Gln Gln Lys Pro

Gly Lys Ala Pro Lys Leu Leu Ile Lys (His Ala Ser Gln Ser Ile Ser) Gly Val Pro Ser

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

Glu Asp Phe Ala Thr Tyr Tyr Cys (Gln Gln Ser Asn Ser Trp Pro Tyr Thr) Phe Gly Gln

Gly Thr Lys Val Glu Ile Lys Arg

Hum I:
VH Domain (SEQ ID NO: 33)
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu

Ser Cys Ala Ala Ser (Gly Phe Asn Ile Lys Asp Thr Tyr Ile His) Trp Met Arg Gln Ala

Pro Gly Lys Gly Leu Glu Trp Val Ala (Arg Ile Asp Pro Ala Asn Asp Asn Thr Ile Tyr Asp Pro

Lys Val Gln Gly) Arg Phe Thr Met Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn

Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Thr (Ser Gly Tyr Trp Phe Ala Tyr) Trp

Gly Gln Gly Thr Leu Val Thr Val Ser Ser

VL Domain (SEQ ID NO: 35)
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr

Ile Thr Cys (Arg Ala Ser Gln Ser Ile Ser Asn Asn Leu His) Trp Tyr Gln Gln Lys Pro

Gly Lys Ala Pro Lys Leu Leu Ile Lys (His Ala Ser Gln Ser Ile Ser) Gly Val Pro Ser

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

Glu Asp Phe Ala Thr Tyr Tyr Cys (Gln Gln Ser Asn Ser Trp Pro Tyr Thr) Phe Gly Gln

Gly Thr Lys Val Glu Ile Lys Arg---